

Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: 2568)

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1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAAGTGAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTTCTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTCCT TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCATAA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC

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Figure 2A. The cDNA (SEQ ID. NO. :2569) and amino acid sequence (SEQ ID. NO. :2570) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.

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1 gccggcctccagcagcgggcgcggcgggcgagcagacccactctcctgcggccgcg
61 ggtggagcagcgcgagcccgccctcgctgagccggcgggggcgaggagatgagttgcggc
121 cccgcggcagcgcgccccaggatggggaggagcgcgcggcactgccctcgagaactggcgct
181 ccggtgaagttaggcgcgcggccgctccgcctcccccaagccgttcgcaccgcggccgcg
1 M A G S G A W K R L K S M L R K
241 tcagcctctgccATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCCGCTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGGCTTTCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGGAAGGCCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAGATTACCTTTGGATTT
177 H R L E V L S A M I S V L L V Y I L M G

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781 CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA
197 F L L Y E A V Q R T I H M N Y E I N G D
841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACATGAAATAAATGGAGAT
217 I M L I T A A V G V A V N V I M G F L L
901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTG
237 N Q S G H R H S H S H S L P S N S P T R
961 AACCAGTCTGGTCACCGTCACTCCCATTTCCCACTCCCTGCCTTCAAATTCCCCTACCAGA
257 G S G C E R N H G Q D S L A V R A A F V
1021 GGTTCCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTGA
277 H A L G D L V Q S V G V L I A A Y I I R
1081 CATGCTTTGGGAGATTGTTGACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGA
297 F K P E Y K I A D P I C T Y V F S L L V
1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG
317 A F T T F R I I W D T V V I I L E G V P
1201 GCTTTTACAACATTTTGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCA
337 S H L N V D Y I K E A L M K I E D V Y S
1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA
357 V E D L N I W S L T S G K S T A I V H I
1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATA
377 Q L I P G S S S K W E E V Q S K A N H L
1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA
397 L L N T F G M Y R C T I Q L Q S Y R Q E
1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAA
417 V D R T C A N C Q S S S P *
1501 GTGGACAGAACTTGTGCAAATTGTCAGAGTTCCTAGTCCCTAAAttttatgtattttgggaa
1561 ctcctgccttattttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatga
1621 gaaaatggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccc
1681 cagcctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcaga
1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag
1801 aagacaatccaagatcatacttcattaacttgacagagtacgtgtcttaaaggaagcatc
1861 aagaattcaatattttgcatttaaaaaatactttttaaggccattttatattaagccagtgc
1921 tggaaaactgaatttttttttattatgtataataatctcgacaccagcttctggaattgc
1981 tgctttctttttacagaaattactacccaacagatttcaggaagtactagtagttatccc
2041 aaaagtgggaataagcatgtattcctaagtgtttcagaaatgttttatttcacacataagt
2101 cttaatgttattgttatgtattatactttataaacaaccttttcagatgctacagggttt
2161 tgaatctcaaagttaacattttttcattatttgaatcttagaaccaaatctttattttatt
2221 gtggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag

2281 ttagtcttaaactcaaattactatatgatgatttaaacaataaaagagcgaggatgg

2341 ggaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :2571) and amino acid sequence (SEQ ID. NO. :2572) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

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1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGACCCGACCCTCCAGGCCGACGATGATTCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAAGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAATCACCAACCAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCACTCCCTGCCTTCAAATTCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
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961 TTTGAATCATATGGGATACAGTAGTTATAATACTAGAAAGGTGTGCCAAGCCATTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaaatggaatc
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt
1441 gctagtcctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc
1501 ccaaacactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. :2573) and amino acid sequence (SEQ ID. NO. :2574) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

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1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAATCACCAACCAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA

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321 F R I I W D T V V I I L E G V P S H L N
961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAttttatgtattgttttagcattgctgaatt
1321 cactttatttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaa
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc
1441 ctgacagtgtctgtctgttttaattggtaaaaggagactttgccataattttcagatgaa
1501 gatgtttcccaaactgtttacagaatgagatgtgactcctacagatacctcatag

Figure 3:

Figure 3A. Amino acid sequence corresponding to 108P5H8 v.1 (SEQ ID NO: 2570) and 108P5H8 v.2 (SEQ ID. NO. :2572). The 108P5H8 v.1 and 108P5H8 v.2 proteins have 429 amino acids.

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1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFD  FSDEAGDEGL  SRFNKL RVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQKRV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAIILTLLA  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVA VNV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAF TT  FRIIWDTVVI  ILEGVP SHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGM YRCTIQL  QSYRQEVDR T
421 CANCQSSSP*

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Figure 3B. Amino acid sequence corresponding to 108P5H8 v.3 (SEQ ID. NO. :2574).
The 108P5H8 v.3 protein has 429 amino acids.

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1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFE  FSDEAGDEGL  SRFNKL RVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQKRV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAIILTLLA  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVA VNV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAF TT  FRIIWDTVVI  ILEGVP SHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGM YRCTIQL  QSYRQEVDR T
421 CANCQSSSP*

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Figure 4:

Figure 4A Nucleic acid sequence alignment of the 3 variants of 108P5H8. (SEQ ID NO: 2573). Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

1	15	16	30	31	45	46	60	61	75	76	90
V.1	CGCGGCTCCAGCAG	CGGGCGCGCGGGCG	CGAGCACGACCCAC	TCTCTGCGCGCGG	GGTGAGCAGCGGA	CGCGGCTCGTGAG					
V.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
V.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
91	105	106	120	121	135	136	150	151	165	166	180
V.1	CCGCGCGGGGCGGG	GAGATGAGTTGCGG	CCGCGGCAGCGCC	CAGGATGGGAGGGA	CGCGGCGACTGCC	TCGAGAACTGGCGCT					
V.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
V.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
181	195	196	210	211	225	226	240	241	255	256	270
V.1	CCGCTGAAGTAGCG	CCGCGGCGCGTCCG	CTCCCCAAGCGTT	CCGACCGCGGCGC	TCAGCCTCTGCCATG	GCCGGCTCTGGCGG					
V.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
V.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
271	285	286	300	301	315	316	330	331	345	346	360
V.1	TGGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCTG	TTTTAAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGCGGGG					
V.2	TGGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCTG	TTTTAAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGCGGGG					
V.3	TGGAAGCGCCTCAA	TCTATGCTAAGGAAG	GATGATGCGCGCTG	TTTTAAATGACACC	AGCGCCTTTGACTTC	TCGGATGAGCGGGG					
361	375	376	390	391	405	406	420	421	435	436	450
V.1	GACGAGGGGCTTCT	CGGTTCAACAACTT	CGAGTTGTTGGTGGC	GATGACGGTTCCGAA	GCCCCGGAAGGCCT	GTTAACGGGGCGCAC					
V.2	GACGAGGGGCTTCT	CGGTTCAACAACTT	CGAGTTGTTGGTGGC	GATGACGGTTCCGAA	GCCCCGGAAGGCCT	GTTAACGGGGCGCAC					
V.3	GACGAGGGGCTTCT	CGGTTCAACAACTT	CGAGTTGTTGGTGGC	GATGACGGTTCCGAA	GCCCCGGAAGGCCT	GTTAACGGGGCGCAC					
451	465	466	480	481	495	496	510	511	525	526	540
V.1	CCGACCCCTCCAGGC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTGACCAACAGT	CAGCTGAGTTGAAG	GTGGACTCCTGTGAC					
V.2	CCGACCCCTCCAGGC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTGACCAACAGT	CAGCTGAGTTGAAG	GTGGACTCCTGTGAC					
V.3	CCGACCCCTCCAGGC	GACGATGATTCCTTA	CTGGACCAAGACTTA	CCTTGACCAACAGT	CAGCTGAGTTGAAG	GTGGACTCCTGTGAC					

541 555 556 570 571 585 586 600 601 615 616 630
V.1 AACTGCAGCAAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC TTGCTTTTTCATGATT
V.2 AACTGCAGCAAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC TTGCTTTTTCATGATT
V.3 AACTGCAGCAAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC TTGCTTTTTCATGATT

631 645 646 660 661 675 676 690 691 705 706 720
V.1 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA AGGCCATCATACTC
V.2 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA AGGCCATCATACTC
V.3 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA AGGCCATCATACTC

721 735 736 750 751 765 766 780 781 795 796 810
V.1 ACCCTGCTTGTCTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT TTGTCAGCTATGATT
V.2 ACCCTGCTTGTCTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT TTGTCAGCTATGATT
V.3 ACCCTGCTTGTCTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT TTGTCAGCTATGATT

811 825 826 840 841 855 856 870 871 885 886 900
V.1 AGTGTGCTGTTGGTG TATATACCTTATGGGA TTCTCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACCTAT GAAATAAATGGAGAT
V.2 AGTGTGCTGTTGGTG TATATACCTTATGGGA TTCTCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACCTAT GAAATAAATGGAGAT
V.3 AGTGTGCTGTTGGTG TATATACCTTATGGGA TTCTCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACCTAT GAAATAAATGGAGAT

901 915 916 930 931 945 946 960 961 975 976 990
V.1 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTTG AACCCAGTCTGGTCAC CGTCACTCCCATTC
V.2 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTTG AACCCAGTCTGGTCAC CGTCACTCCCATTC
V.3 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTTG AACCCAGTCTGGTCAC CGTCACTCCCATTC

991 1005 1006 1020 1021 1035 1036 1050 1051 1065 1066 1080
V.1 CACTCCCTGCCTTCA AATCCCTTACCAGA GGTTCCTGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG AGAGCTGCATTGTA
V.2 CACTCCCTGCCTTCA AATCCCTTACCAGA GGTTCCTGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG AGAGCTGCATTGTA
V.3 CACTCCCTGCCTTCA AATCCCTTACCAGA GGTTCCTGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG AGAGCTGCATTGTA

1081 1095 1096 1110 1111 1125 1126 1140 1141 1155 1156 1170
V.1 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC AAGATTGCTGACCCC
V.2 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC AAGATTGCTGACCCC
V.3 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC AAGATTGCTGACCCC

1171 1185 1186 1200 1201 1215 1216 1230 1231 1245 1246 1260
V.1 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC AAGATTGCTGACCCC
V.2 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC AAGATTGCTGACCCC
V.3 CATGCTTTGGGAGAT TTGGTACAGAGTGT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC AAGATTGCTGACCCC

v.1 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA CTAGAAGGTGTGCCA
v.2 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA CTAGAAGGTGTGCCA
v.3 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA CTAGAAGGTGTGCCA

1261 1275 1276 1290 1291 1305 1306 1320 1321 1335 1336 1350
v.1 AGCCATTGTGAATGTA GACTATATCAAAAGAA GCCTTGATGAAATA GAAGATGTATATTCA GTGGAAGATTAAAT ATCTGGTCTCTCACT
v.2 AGCCATTGTGAATGTA GACTATATCAAAAGAA GCCTTGATGAAATA GAAGATGTATATTCA GTGGAAGATTAAAT ATCTGGTCTCTCACT
v.3 AGCCATTGTGAATGTA GACTATATCAAAAGAA GCCTTGATGAAATA GAAGATGTATATTCA GTGGAAGATTAAAT ATCTGGTCTCTCACT

1351 1365 1366 1380 1381 1395 1396 1410 1411 1425 1426 1440
v.1 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCATCTAAATGG GAGGAAGTACAGTCC AAAGCAAACCATTTA
v.2 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCATCTAAATGG GAGGAAGTACAGTCC AAAGCAAACCATTTA
v.3 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCATCTAAATGG GAGGAAGTACAGTCC AAAGCAAACCATTTA

1441 1455 1456 1470 1471 1485 1486 1500 1501 1515 1516 1530
v.1 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT GCAAAATTGTCAGAGT
v.2 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT GCAAAATTGTCAGAGT
v.3 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT GCAAAATTGTCAGAGT

1531 1545 1546 1560 1561 1575 1576 1590 1591 1605 1606 1620
v.1 TCTAGTCCCTAAATTT TATGTATT TTGGG AACTCCTG-----C GTTATTTATCCTGCA GTCACAGACTTGAGA GCAATAAATGCAAAC
v.2 TCTAGTCCCTAAATTT TATGTATT TTGGG GACTCCTG-----C GTTATTTATCCTGCA GTCACAGACTTGAGA GCAATAAATGCAAAC
v.3 TCTAGTCCCTAAATTT TATGTATTGTTTGTAG CAJTGCTGAATTTCAC TTTATTTATCCTGCA GTCACAGACTTGAGA GCAATAAATGCAAAC

1621 1635 1636 1650 1651 1665 1666 1680 1681 1695 1696 1710
v.1 CTAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG ACAGTGTAGTCTCT
v.2 CTAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG ACAGTGTAGTCTCT
v.3 CTAATGAGAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG ACAGTGTAGTCTCT

1711 1725 1726 1740 1741 1755 1756 1770 1771 1785 1786 1800
v.1 GTTTAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAACACTG TTTACAGAATGAGAT GTGACTCTTACAGAT
v.2 GTTTAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAACACTG TTTACAGAATGAGAT GTGACTCTTACAGAT
v.3 GTTTAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAACACTG TTTACAGAATGAGAT GTGACTCTTACAGAT

1801 1815 1816 1830 1831 1845 1846 1860 1861 1875 1876 1890

100024652 100000000

v.1 ACCTCATAGAGACA ATCCAGATCATACT TCATTAACTTGACAG AGTACGTGCTTTAA GGAAGCATCAAGAAT TCAATATTTGCATTT
 v.2 ACCTCATAG-----
 v.3 ACCTCATAG-----

 1891 1905 1906 1920 1921 1935 1936 1950 1951 1965 1966 1980
 v.1 AAAAATACTTTTTAA GGCCATTTTATATTA AGCCAGTGTGGAAA ACTGAATTTTTTTA TTATGTATAATAATC TCGACACCCAGCTTC
 v.2 -----
 v.3 -----

 1981 1995 1996 2010 2011 2025 2026 2040 2041 2055 2056 2070
 v.1 TCGAATTGCTGCTTT CTTTTTACAGAAAT ACTACCAACAGATT TCAGGAAGTACTAGT AGTTATCCCAAAAGT GGAATAAGCATGTAT
 v.2 -----
 v.3 -----

 2071 2085 2086 2100 2101 2115 2116 2130 2131 2145 2146 2160
 v.1 TCCTAAGTGTTCAG AAATGTTTTTATTCA CACAATAAGTCTTAAT GTTATTGTTATGATT ATACTTTATAAACA CCCTTTCCAGATGCT
 v.2 -----
 v.3 -----

 2161 2175 2176 2190 2191 2205 2206 2220 2221 2235 2236 2250
 v.1 ACAGGGTTTTGAATC TCAAAGTTAACATTT TTCAATTATTGTAAT CTTAGAACCATAATCT TTATTTATTGTGGTC ACTGTTATTAAATGA
 v.2 -----
 v.3 -----

 2251 2265 2266 2280 2281 2295 2296 2310 2311 2325 2326 2340
 v.1 TTTAGGAAATACTTT CAATATTATTCTGAA TGGCTGAAGTTAGTC TTAAACTCAAATTAC TATATGATGATTTAA AACAAAATAAAAGAG
 v.2 -----
 v.3 -----

 2341 2355 2356 2370
 v.1 CGAGGATGGGAAAA AAAAAAAAAAAAAA AAA 2364
 v.2 ----- 1548
 v.3 ----- 1557

Figure 4B Amino Acid Alignment of the 3 variants of 108P5H8 (SEQ ID NOS: 2570 & 2572)

1	15	16	30	31	45	46	60	61	75	76	90
V.1	MAGSGAWKRLKSMRL	KDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVADGSEAPER	PVNGAHTLQADDD	LLDQDLPLTNSQLSL					
V.2	MAGSGAWKRLKSMRL	KDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVADGSEAPER	PVNGAHTLQADDD	LLDQDLPLTNSQLSL					
V.3	MAGSGAWKRLKSMRL	KDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVADGSEAPER	PVNGAHTLQADDD	LLDQDLPLTNSQLSL					
91	105	106	120	121	135	136	150	151	165	166	180
V.1	KVDSCDNCSKQREIL	KQKVKAHLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIIITLLALWLSS	KSPTKRFTFGFHRLE					
V.2	KVDSCDNCSKQREIL	KQKVKAHLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIIITLLALWLSS	KSPTKRFTFGFHRLE					
V.3	KVDSCDNCSKQREIL	KQKVKAHLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIIITLLALWLSS	KSPTKRFTFGFHRLE					
181	195	196	210	211	225	226	240	241	255	256	270
V.1	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDLSA					
V.2	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDLSA					
V.3	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT	RGSGCERNHGQDLSA					
271	285	286	300	301	315	316	330	331	345	346	360
V.1	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDIYIK	EALMKIEDVYSVEDL					
V.2	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDIYIK	EALMKIEDVYSVEDL					
V.3	VRAAFVHALGDLVQS	VGVLIAAYIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDIYIK	EALMKIEDVYSVEDL					
361	375	376	390	391	405	406	420	421			
V.1	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	SKANHLLNTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						
V.2	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	SKANHLLNTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						
V.3	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	SKANHLLNTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP						

10004652 : 0570000

Figure 25: Alignment of 108P5H8 v.1 protein with members of the zinc transporter family.

A-Alignment of 108P5H8 (SEQ ID NO:2576) with the human zinc transporter 4, i.e. gi 11432533 (SEQ ID NO: 2577)

Identities = 429/429 (100%), Positives = 429/429 (100%)

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108P5: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
          MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER
Sbjct: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61   PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120
          PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL
Sbjct: 61   PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120

108P5: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
          YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE
Sbjct: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240
          VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG
Sbjct: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240

108P5: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
          HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE
Sbjct: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301  YKIADPICTYVFSLLVAFTTFRIIWDTVVILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
          YKIADPICTYVFSLLVAFTTFRIIWDTVVILEGVPSHLNVDYIKEALMKIEDVYSVEDL
Sbjct: 301  YKIADPICTYVFSLLVAFTTFRIIWDTVVILEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361  NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR 420
          NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR
Sbjct: 361  NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNTFGMYRCTIQLQSYRQEVDR 420

108P5: 421  CANCQSSSP 429
          CANCQSSSP
Sbjct: 421  CANCQSSSP 429

```

B-Alignment of 108P5H8 (SEQ ID NO: 2578) with the human zinc transporter ZNT4, i.e. gi 8134840 (SEQ ID NO: 2579)

Identities = 428/429 (99%), Positives = 429/429 (99%)

```

108P5: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
          MAGSGAWKRLKSMRLRKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER
Sbjct: 1   MAGSGAWKRLKSMRLRKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61   PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120
          PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL
Sbjct: 61   PVNGAHPTLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120

108P5: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
          YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE
Sbjct: 121  YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240
          VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG
Sbjct: 181  VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240

108P5: 241  HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
          HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE

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Sbjct: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL

Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420
NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR

Sbjct: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429
CANCQSSSP

Sbjct: 421 CANCQSSSP 429

C-Alignment of 108P5H8 (SEQ ID NO: 2580) with the rat zinc transporter ZNT-4, i.e. gi 8134837 (SEQ ID NO: 2581).

Identities = 387/430 (90%), Positives = 407/430 (94%), Gaps = 3/430 (0%)

108P5: 1 MAGSGAWKRLKSMRLRKDDAPLFLNDTSADFSDSDEAGDEGLSRFNKLRVAVVADDGSEAPER 60
MAG GAWKRLKS+LRKDDAPLFLNDTSADF DE DEGLSRFNKLRVAVVADD SEAPER

Sbjct: 1 MAGPGAWKRLKSLLRKDDAPLFLNDTSADFDFLDEVSDEGLSRFNKLRVAVVADDSEAPER 60

108P5: 61 PVNGAHP TLQADDDSLDQDLPLTNSQLSLKVDSCDNCCKQREILKQKVKARLTIAAVL 120
PVNGAHP LQADDDSLDQ+LPLTNSQLSLK+D CDNCCK+RE+LKQKVK RLTIAAVL

Sbjct: 61 PVNGAHPALQADDDSLDQELPLTNSQLSLKMDPCDNCCKRRELLKQKVKTRLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
YLLFMIGELVGGY+ANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPT+RFTFGFHRLE

Sbjct: 121 YLLFMIGELVGGYMANSLAIMTDALHMLTDL SAI ILTLLALWLSSKSPTRRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQ-- 238
VLSAMISV+LVY+LMGFLLYE+QRTIHMNYEINGD+MLITAAGVAVNVIMGFLLNQ

Sbjct: 181 VLSAMISVMLVYVLMGFLLYEAMQRTIHMNYEINGDVMLITAAGVAVNVIMGFLLNQSG 240

108P5: 239 SGHRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 298
H H+HSHSLPSNSP+ S +HGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK

Sbjct: 241 HHHSHSHSHSLPSNSPSMVSS-GHSHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 299

108P5: 299 PEYKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVE 358
PEYKIADPICTY+FSLLVAFTT RIIWDTVVILLEGVPSHLNVDYIKE+LMKIEDVYSVE

Sbjct: 300 PEYKIADPICTYIFSLVAFTTLRIIWDTVVILLEGVPSHLNVDYIKESLMKIEDVYSVE 359

108P5: 359 DLNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEV 418
DLNIWSLTSGK+TAIVH+QLIPGSSSKWEEVQSKA HLLLNFTFGMY+CT+QLQSYRQE

Sbjct: 360 DLNIWSLTSGKATAIVHMQIPGSSSKWEEVQSKAKHLLLNFTFGMYKCTVQLQSYRQEAT 419

108P5: 419 RTCANCQSSS 428
RTCANCQSSS

Sbjct: 420 RTCANCQSSS 429

Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: ~~2568~~)

```

1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAAGTAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTTCCTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTCCT TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCTATA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC

```

Figure 2A. The cDNA (SEQ ID. NO. : ~~2569~~) and amino acid sequence (SEQ ID. NO. : ~~2570~~) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.

```

1 gccggcctccagcagcgggcgggcgggcgagcagacccccactctcctgcgggcgcg
61 ggtggagcagcgcgagcccgctcgctgagccggcgggggcggggagatgagttgcggc
121 ccgcggcagcgcggccaggatggggagggagcgcggcactgccctcgagaactggcgct
181 ccggtgaagtaggcgcgcggcgccgtccgcctcccccaagccgttccgcaccgcggcgcg
1      M A G S G A W K R L K S M L R K
241 tcagcctctgccATGGCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCGCTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGCTTTCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGGAAGGCCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGTCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTT
177 H R L E V L S A M I S V L L V Y I L M G

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781 CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA
197 F L L Y E A V Q R T I H M N Y E I N G D
841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGAT
217 I M L I T A A V G V A V N V I M G F L L
901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTG
237 N Q S G H R H S H S H S L P S N S P T R
961 AACCAGTCTGGTCACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCCTACCAGA
257 G S G C E R N H G Q D S L A V R A A F V
1021 GGTTCCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTGA
277 H A L G D L V Q S V G V L I A A Y I I R
1081 CATGCTTTGGGAGATTGTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGA
297 F K P E Y K I A D P I C T Y V F S L L V
1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG
317 A F T T F R I I W D T V V I I L E G V P
1201 GCTTTTACAACATTTTGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCA
337 S H L N V D Y I K E A L M K I E D V Y S
1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA
357 V E D L N I W S L T S G K S T A I V H I
1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATA
377 Q L I P G S S S K W E E V Q S K A N H L
1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA
397 L L N T F G M Y R C T I Q L Q S Y R Q E
1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAA
417 V D R T C A N C Q S S S P *
1501 GTGGACAGAACTTGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttgggaa
1561 ctccctgccttattttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatga
1621 gaaaatggaatccctgacagctgtgtccgatcaagcatcagtcctctcaaacagttgccc
1681 cagcctgacagtgctagtcctgttttaattggtaaaaggagactttgccataattttcaga
1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag
1801 aagacaatccaagatcatacttcattaacttgacagagtagctgtcttaaaggaagcatc
1861 aagaattcaatattttgcatttaaaaaataactttttaaggccattttatattaagccagtgc
1921 tggaaaactgaattttttttattatgtataataatctcgacaccagcttctggaattgc
1981 tgctttctttttacagaaattactaccaacagatttcaggaagtactagtagttatccc
2041 aaaagtgggaataagcatgtatttcctaagtgtttcagaaatgttttatttcacacataagt
2101 cttaatgttattgttatgattatactttataaacaaccttttcagatgctacagggttt
2161 tgaatctcaaagttaacattttttcattatttgtaatcttagaaccaaatctttattttatt
2221 gtgggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag

~~City Docket: 511582002500~~

2281 ttagtcttaaactcaaattactatatgatgatttaaacaataaaaagagcgaggatgg
2341 ggaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :257) and amino acid sequence (SEQ ID. NO. :257) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTAAACGGGGCGACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAAGCTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCACTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
```

961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaaatggaatc
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt
1441 gctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc
1501 ccaaacactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. : ~~2573~~) and amino acid sequence (SEQ ID. NO. : ~~2574~~) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```
1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTCACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCTCCCTGCCTTCAAATTCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
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~~File Docket: 511582002500~~

321 F R I I W D T V V I I L E G V P S H L N
961 TTTGGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAttttatgtattgttttagcattgctgaatt
1321 cactttatttatectgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaa
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc
1441 ctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaa
1501 gatgtttcccaaactgtttacagaatgagatgtgactcctacagatacctcatag

Figure 3:

(SEQ ID NO 2570)

Figure 3A. Amino acid sequence corresponding to 108P5H8 v.1 and 108P5H8 v.2 (SEQ ID. NO. 2572). The 108P5H8 v.1 and 108P5H8 v.2 proteins have 429 amino acids.

```

1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFD  FSDEAGDEGL  SRFNKLRRVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQRKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILLTLLA  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVAENV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL  A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAF  TT  FRIIWDTVVI  ILEGVPSHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGMYRCTIQL  QSYRQEVDR  T
421  CANCQSSSP*

```

Figure 3B. Amino acid sequence corresponding to 108P5H8 v.3 (SEQ ID. NO. 2574). The 108P5H8 v.3 protein has 429 amino acids.

```

1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFE  FSDEAGDEGL  SRFNKLRRVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSLDDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQRKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILLTLLA  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVAENV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL  A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAF  TT  FRIIWDTVVI  ILEGVPSHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGMYRCTIQL  QSYRQEVDR  T
421  CANCQSSSP*

```

Figure 4:

(SER ID NO: 2573)

Figure 4A Nucleic acid sequence alignment of the 3 variants of 108P5H8A. Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

[illegible]

271 285 286 300 301 315 316 330 331 345 346

360

v.1 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGGCCGCTG TTTTAAATGACACC AGGCGCTTTGACTTC
TCGGATGAGCGGGG
v.2 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGGCCGCTG TTTTAAATGACACC AGGCGCTTTGACTTC
TCGGATGAGCGGGG
v.3 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGGCCGCTG TTTTAAATGACACC AGGCGCTTTGACTTC
TCGGATGAGCGGGG

361 375 376 390 391 405 406 420 421 435 436

450

v.1 GACGAGGGGCTTTCT CGGTTCAACAAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT
GTTAACGGGGCGCAC
v.2 GACGAGGGGCTTTCT CGGTTCAACAAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT
GTTAACGGGGCGCAC
v.3 GACGAGGGGCTTTCT CGGTTCAACAAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT
GTTAACGGGGCGCAC

451 465 466 480 481 495 496 510 511 525 526

540

v.1 CCGACCCCTCCAGGCC GACGATGATTCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG
GTGGACTCCTGTGAC
v.2 CCGACCCCTCCAGGCC GACGATGATTCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG
GTGGACTCCTGTGAC
v.3 CCGACCCCTCCAGGCC GACGATGATTCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG
GTGGACTCCTGTGAC

541 555 556 570 571 585 586 600 601 615 616

630

v.1 AACTGCAGCAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGTTGACCAATT GCTGCCGTTCTGTAC
TTGCTTTTCATGATT

V.2 AACTGCAGCAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC
TTGCTTTTCATGATT
V.3 AACTGCAGCAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCATT GCTGCCGTTCTGTAC
TTGCTTTTCATGATT

631 645 646 660 661 675 676 690 691 705 706

720 V.1 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCCTA
AGCGCCATCATACTC
V.2 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCCTA
AGCGCCATCATACTC
V.3 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCCTA
AGCGCCATCATACTC

721 735 736 750 751 765 766 780 781 795 796

810 V.1 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT
TTGTCAGCTATGATT
V.2 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT
TTGTCAGCTATGATT
V.3 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACCAAAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT
TTGTCAGCTATGATT

811 825 826 840 841 855 856 870 871 885 886

900 V.1 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT
GAAATAAATGGAGAT
V.2 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT
GAAATAAATGGAGAT
V.3 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCCTCTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT
GAAATAAATGGAGAT

10004652 061000

976

961

946

931

916

901

990

ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTGTTG AACCAAGCTCTGGTCAC
 v.1
 CGTCACTCCCATTTCC
 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTGTTG AACCAAGCTCTGGTCAC
 v.2
 CGTCACTCCCATTTCC
 ATAATGCTCATCACC GCAGCTGTTGGAGTT GCAGTTAATGTAATA ATGGGGTTTCTGTGTTG AACCAAGCTCTGGTCAC
 v.3
 CGTCACTCCCATTTCC

1065

1051

1036

1021

1006

991

1066

1080

CACTCCCTGCCTTCA AATTCCCCTACCAGA GGTCTGGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG
 v.1
 AGAGCTGCATTTGTA
 CACTCCCTGCCTTCA AATTCCCCTACCAGA GGTCTGGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG
 v.2
 AGAGCTGCATTTGTA
 CACTCCCTGCCTTCA AATTCCCCTACCAGA GGTCTGGGTGTGAA CGTAACCATGGGCAG GATAGCCTGGCAGTG
 v.3
 AGAGCTGCATTTGTA

1155

1141

1126

1111

1096

1081

1156

1170

CATGCTTTGGGAGAT TTGGTACAGAGTGTT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC
 v.1
 AAGATTGCTGA~~CCCC~~
 CATGCTTTGGGAGAT TTGGTACAGAGTGTT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC
 v.2
 AAGATTGCTGA~~TCCC~~
 CATGCTTTGGGAGAT TTGGTACAGAGTGTT GGTGTGCTAATAGCT GCATACATCATACGA TTCAAGCCAGAAATAC
 v.3
 AAGATTGCTGA~~CCCC~~

1245

1231

1216

1201

1186

1171

1246

1260

ATCTGTACATACGTA TTTTCATTACTTGTG GCCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA
 v.1
 CTAGAAGGTGTGCCA

110004552 1000000000

V.2 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA
CTAGAAGGTGTGCCA
V.3 ATCTGTACATACGTA TTTTCATTACTTGTG GCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA
CTAGAAGGTGTGCCA

1261 1275 1276 1290 1291 1305 1306 1320 1321 1335
1336 1350
V.1 AGCCATTGGAATGTA GACTATATCAAAGAA GCCTTGATGAAAATA GAAGATGTATATTCA GTCGAAGATTTTAAAT
ATCTGGTCTCTCACT
V.2 AGCCATTGGAATGTA GACTATATCAAAGAA GCCTTGATGAAAATA GAAGATGTATATTCA GTCGAAGATTTTAAAT
ATCTGGTCTCTCACT
V.3 AGCCATTGGAATGTA GACTATATCAAAGAA GCCTTGATGAAAATA GAAGATGTATATTCA GTCGAAGATTTTAAAT
ATCTGGTCTCTCACT

1351 1365 1366 1380 1381 1395 1396 1410 1411 1425
1426 1440
V.1 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCAATCTAAATGG GAGGAAGTACAGTCC
AAAGCAAACCATTTA
V.2 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCAATCTAAATGG GAGGAAGTACAGTCC
AAAGCAAACCATTTA
V.3 TCAGGAAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCAATCTAAATGG GAGGAAGTACAGTCC
AAAGCAAACCATTTA

1441 1455 1456 1470 1471 1485 1486 1500 1501 1515
1516 1530
V.1 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT
GCAAAATTGTCAGAGT
V.2 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT
GCAAAATTGTCAGAGT
V.3 TTATTGAACACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT
GCAAAATTGTCAGAGT

1606	1531	1545	1546	1560	1561	1575	1576	1590	1591	1605	
	v.1	TCTAGTCCCTAA	TTT	TATGTATT	--TTGGG	AACTCCTG	----	C	CTTATT	TATCCTTGCA	GTCACAGACTTGAGA
		GCAATAAAATGCA	AAAC								
	v.2	TCTAGTCCCTAA	TTT	TATGTATT	--TTGGG	GACTCCTG	----	C	CTTATT	TATCCTTGCA	GTCACAGACTTGAGA
		GCAATAAAATGCA	AAAC								
	v.3	TCTAGTCCCTAA	TTT	TATGTATT	GTGTTTAG	CATGCTGAATT	TCAC		TTTATT	TATCCTTGCA	GTCACAGACTTGAGA
		GCAATAAAATGCA	AAAC								

[illegible]

	1711	1725	1726	1740	1741	1755	1756	1770	1771	1785
1786	1800									
	v.1	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	TTTTCCCAACACTG	TTTTACAGAATGAGAT				
		GTGACTC-TACAGAT								
	v.2	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	TTTTCCCAACACTG	TTTTACAGAATGAGAT				
		GTGACTC-TACAGAT								
	v.3	GTTTAATGGTAAAAG	GAGACTTTGCCATAA	TTTTTCAGATGAAGAT	TTTTCCCAACACTG	TTTTACAGAATGAGAT				
		GTGACTC-TACAGAT								

```

1876      1801      1815 1816      1830 1831      1845 1846      1860 1861      1875
          1890
v.1 ACCTCATAGAAGACA ATCCAAGATCATACT TCATTAACTTGACAG AGTACGTGTCTTAA GGAAGCATCAAGAAT
TCAATATTGCAATTT

```

V.2 ACCTCATAG-----

 V.3 ACCTCATAG-----

 1966 1891 1905 1906 1920 1921 1935 1936 1950 1951 1965
 1980
 V.1 AAAAATACTTTTAA GGCCATTTTATATTA AGCCAGTGTGAAA ACTGAATTTTTTTTA TTATGTATAATAATC
 TCGACACCCAGCTTC
 V.2 -----

 V.3 -----

 2056 1981 1995 1996 2010 2011 2025 2026 2040 2041 2055
 2070
 V.1 TGAATGTGCTTTT CTTTTACAGAAATT ACTACCAACAGATT TCAGGAAGTACTAGT AGTTATCCCAAAAGT
 GGAATAAGCATGTAT
 V.2 -----

 V.3 -----

 2146 2071 2085 2086 2100 2101 2115 2116 2130 2131 2145
 2160
 V.1 TCCTAAGTGTTCAG AAATGTTTTTATTCA CACATAAGTCTTAAT GTTATTGTTATGATT ATACTTTATAAACAA
 CCTTTCCAGATGCT
 V.2 -----

 V.3 -----

10024652, 063802

2161 2175 2176 2190 2191 2205 2206 2220 2221 2235 2236
2250
V.1 ACAGGGTTTGAATC TCAAAGTTAACATTT TTCATTATTGTAAT CTTAGAACCAAATCT TTATTATTGTGGTC
ACTGTTATTAAATGA
V.2 -----

V.3 -----

2251 2265 2266 2280 2281 2295 2296 2310 2311 2325
2326 2340
V.1 TTTAGGAAATACTTT CAATATTATTCTGAA TGGCTGAAGTTAGTC TTAAACTCAAATTAC TATATGATGATTAA
AACAAAATAAAAGAG
V.2 -----

V.3 -----

2341 2355 2356 2370
V.1 CGAGGATGGGAAAA AAAAAAAAAAAAAA AAA 2364
V.2 ----- 1548
V.3 ----- 1557

10004552 10659062

Figure 4B Amino Acid Alignment of the 3 variants of 108P5H8

1	15	16	30	31	45	46	60	61	75
76	90								
v.1	MAGSGAWKRLKSMRLR	KDDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHP	TLQADDD			
	LLDQDLPLTNSQLSL								
v.2	MAGSGAWKRLKSMRLR	KDDAPLFLNDTSAFD	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHP	TLQADDD			
	LLDQDLPLTNSQLSL								
v.3	MAGSGAWKRLKSMRLR	KDDAPLFLNDTSAFE	FSDEAGDEGLSRFNK	LRVVVADDGSEAPER	PVNGAHP	TLQADDD			
	LLDQDLPLTNSQLSL								
166	91	105	106	120	121	135	136	150	151
	180								165
v.1	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIILTLLALWLSS				
	KSPTKRFTFGFHRLE								
v.2	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIILTLLALWLSS				
	KSPTKRFTFGFHRLE								
v.3	KVDSCDNCCKQREIL	KQKVKARLTIAAVL	YLLFMIGELVGGYIA	NSLAIMTDALHMLTD	LSAIILTLLALWLSS				
	KSPTKRFTFGFHRLE								
256	181	195	196	210	211	225	226	240	241
	270								255
v.1	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAVG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT				
	RGSGCERNHGQDLSA								
v.2	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAVG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT				
	RGSGCERNHGQDLSA								
v.3	VLSAMISVLLVYILM	GFLLYEAVQRTIHMN	YEINGDIMLITAAVG	VAVNVIMGFLLNQSG	HRHSHSHSLPSNSPT				
	RGSGCERNHGQDLSA								
346	271	285	286	300	301	315	316	330	331
	360								345

V.1 VRAAFVHALGDLVQS VGVLIAAYIIRFKPE YKIADPCTYVFSLL VAFTRRIIWDTVVI ILEGVPSHLNVDYIK
EALMKIEDVYSVEDL
V.2 VRAAFVHALGDLVQS VGVLIAAYIIRFKPE YKIADPCTYVFSLL VAFTRRIIWDTVVI ILEGVPSHLNVDYIK
EALMKIEDVYSVEDL
V.3 VRAAFVHALGDLVQS VGVLIAAYIIRFKPE YKIADPCTYVFSLL VAFTRRIIWDTVVI ILEGVPSHLNVDYIK
EALMKIEDVYSVEDL

361	375	376	390	391	405	406	420	421	
V.1	NIWSLTSGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP				429
V.2	NIWSLTSGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP				429
V.3	NIWSLTSGKSTAIHV	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CANCQSSSP				429

10024652 . 062302

Figure 25: Alignment of 108P5H8 v.1 protein with members of the zinc transporter family.

(SEQ ID NO: 2576)

A-Alignment of 108P5H8 with the human zinc transporter 4, i.e. gi 11432533

(SEQ ID NO: 2577)

Identities = 429/429 (100%), Positives = 429/429 (100%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER
 Sbjct: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120
 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL
 Sbjct: 61 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE
 Sbjct: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGAVNVIMGFLNQS G 240
 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGAVNVIMGFLNQS G
 Sbjct: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGAVNVIMGFLNQS G 240

108P5: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE
 Sbjct: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVV IILEGVPSHLNVDYI KEALMKIEDVYSVEDL 360
 YKIADPICTYVFSLLVAFTTFRIIWDTVV IILEGVPSHLNVDYI KEALMKIEDVYSVEDL
 Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVV IILEGVPSHLNVDYI KEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAI VHIQLIPGSSSKWEEVQSKANHLLLN TFGMYRCTIQLQSYRQEVDR T 420
 NIWSLTSGKSTAI VHIQLIPGSSSKWEEVQSKANHLLLN TFGMYRCTIQLQSYRQEVDR T
 Sbjct: 361 NIWSLTSGKSTAI VHIQLIPGSSSKWEEVQSKANHLLLN TFGMYRCTIQLQSYRQEVDR T 420

108P5: 421 CANCQSSSP 429
 CANCQSSSP
 Sbjct: 421 CANCQSSSP 429

(SEQ ID NO: 2578)

B-Alignment of 108P5H8 with the human zinc transporter ZNT4, i.e. gi 8134840

(SEQ ID NO: 2579)

Identities = 428/429 (99%), Positives = 429/429 (99%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
 MAGSGAWKRLKSMRLKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER
 Sbjct: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120
 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL
 Sbjct: 61 PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQKVKARLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE
 Sbjct: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGAVNVIMGFLNQS G 240
 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGAVNVIMGFLNQS G
 Sbjct: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGAVNVIMGFLNQS G 240

108P5: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE
 Sbjct: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
 YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL
 Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420
 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR
 Sbjct: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429
 CANCQSSSP
 Sbjct: 421 CANCQSSSP 429

(seq ID No: 2580)

C-Alignment of 108P5H8₄ with the rat zinc transporter ZNT-4, i.e. gi 8134837 (seq ID No: 2581)

Identities = 387/430 (90%), Positives = 407/430 (94%), Gaps = 3/430 (0%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFDFDEAGDEGLSRFNKLRVVVADDGSEAPER 60
 MAG GAWKRLKS+LRKDDAPLFLNDTSADF DE DEGLSRFNKLRVVVADD SEAPER
 Sbjct: 1 MAGPGAWKRLKSLLRKDDAPLFLNDTSADFDFLDEVSEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61 PVNGAHP TLQADDDSLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL 120
 PVNGAHP LQADDDSLDQ+LPLTNSQLSLK+D CDNCSK+RE+LKQRKVK RL TIAAVL
 Sbjct: 61 PVNGAHPALQADDDSLDQELPLTNSQLSLKMDPCDNCSKRRELLKQRKVKRLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
 YLLFMIGELVGGY+ANS LAIMTDALHMLTDLSAI ILTLLALWLSSKSPT+RFTFGFHRLE
 Sbjct: 121 YLLFMIGELVGGYMANSLAIMTDALHMLTDLSAI ILTLLALWLSSKSPTRRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAVGAVNVIMGFLLNQ-- 238
 VLSAMISV+LVY+LMGFLLYE+QRTIHMNYEINGD+MLITAAVGAVNVIMGFLLNQ
 Sbjct: 181 VLSAMISVMLVYVLMGFLLYEAMQRTIHMNYEINGDVMLITAAVGAVNVIMGFLLNQSG 240

108P5: 239 SGHRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 298
 H H+HSHSLPSNSP+ S +HGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK
 Sbjct: 241 HHHSHSHSHSLPSNSPSMVSS-GHSHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 299

108P5: 299 PEYKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVE 358
 PEYKIADPICTY+FSLLVAFTT RIIWDTVVIIIEGVPSHLNVDYIKE+LMKIEDVYSVE
 Sbjct: 300 PEYKIADPICTYIFSLVAFTTLRIIWDTVVIIIEGVPSHLNVDYIKESLMKIEDVYSVE 359

108P5: 359 DLNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEV 418
 DLNIWSLTSGK+TAIVH+QLIPGSSSKWEEVQSKA HLLLNFTFGMY+CT+QLQSYRQE
 Sbjct: 360 DLNIWSLTSGKATAIVHMLIPGSSSKWEEVQSKAKHLLLNFTFGMYKCTVQLQSYRQEAT 419

108P5: 419 RTCANCQSSS 428
 RTCANCQSSS
 Sbjct: 420 RTCANCQSSS 429